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3M protein - protein search, using sw model

Run on: September 4, 2002, 17:32:06 ; Search time 29.8 seconds
(without alignments)
108.092 Million cell updates/sec

Title: US-09-202-035-39

Profile score: 169

Sequence: 1 KORONKPPSKPNDHFVFNFVPCISICG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	163	96.4	29	19	AAW39247	Human RSV G protei
2	163	96.4	42	19	AAW39245	Human RSV A subtyp
3	163	96.4	49	19	AAW39217	Human RSV A subtyp
4	163	96.4	49	19	AAW39219	Human RSV A subtyp
5	163	96.4	49	19	AAW39224	Human RSV G protei
6	163	96.4	49	19	AAW39244	Human RSV G protei
7	163	96.4	49	19	AAW39248	Human RSV G protei
8	163	96.4	49	19	AAW39250	Human RSV G protei
9	163	96.4	49	19	AAW39251	Human RSV G protei
10	163	96.4	298	8	AAW70845	Sequence of human
11	163	96.4	298	13	AAW25302	HSRV glycoprotein

12	163	96.4	298	19	AAW47605	HSRV glycoprotein
13	163	96.4	581	10	AAW90441	Chimeric human res
14	160	94.7	49	19	AAW39218	Human RSV A subtyp
15	160	94.7	49	19	AAW39221	Human RSV A subtyp
16	160	94.7	49	19	AAW39222	Human RSV A subtyp
17	160	94.7	49	19	AAW39223	Human RSV A subtyp
18	160	94.7	51	17	AAW97077	Respiratory Syncyt
19	160	94.7	51	20	AAW44104	RSV G protein anti
20	160	94.7	53	17	AAW84149	Amno acid sequenc
21	160	94.7	53	17	AAW97076	Respiratory Syncyt
22	160	94.7	53	20	AAW44103	RSV G protein anti
23	160	94.7	53	22	AAW84148	Amno acid sequenc
24	160	94.7	55	17	AAW97075	Respiratory Syncyt
25	160	94.7	55	20	AAW44102	RSV G protein anti
26	160	94.7	55	22	AAW84147	Amno acid sequenc
27	160	94.7	57	17	AAW97074	Respiratory Syncyt
28	160	94.7	57	20	AAW44101	RSV G protein anti
29	160	94.7	57	22	AAW84146	Amno acid sequenc
30	160	94.7	59	17	AAW97073	Respiratory Syncyt
31	160	94.7	59	20	AAW44100	RSV G protein anti
32	160	94.7	59	22	AAW84145	Amno acid sequenc
33	160	94.7	61	17	AAW97072	Respiratory Syncyt
34	160	94.7	61	20	AAW44099	RSV G protein anti
35	160	94.7	61	22	AAW84144	Amno acid sequenc
36	160	94.7	101	16	AAW88253	RSV subgroup A w11
37	160	94.7	101	17	AAW95610	RSV subgroup A prote
38	160	94.7	101	17	AAW95616	RSV sub-group A w1
39	160	94.7	101	17	AAW97050	Respiratory Syncyt
40	160	94.7	101	20	AAW44078	RSV G protein anti
41	160	94.7	101	20	AAW97310	Peptide which indu
42	160	94.7	101	21	AAW18805	A G2Na peptide der
43	160	94.7	101	22	AAW67741	Amno acid sequenc
44	160	94.7	101	22	AAW84123	Amno acid sequenc
45	160	94.7	101	22	AAW68016	Amno acid sequenc

ALIGNMENTS

RESULT 1

AAW39247
ID AAW39247 standard; peptide: 29 AA.
AC AAW39247;
XX
DT 27-AUG-1998 (first entry)
XX
DE Human RSV G protein fragment (aa. 149-157) derivative #4.
XX
KW G protein; treatment: diagnosis; infection; immunity;
KW antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
OS Human respiratory syncytial virus.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="N-terminal acetylated"
FT FT /note="C-terminal amide"
FT Modified-site 29 /note="C-terminal amide"
XX
PN W09746581-A1.
XX
PD 11-DEC-1997.
XX
PF 04-JUN-1997; 97W0-AU00351.
XX
PR 05-JUN-1996; 96AU-0000265.
XX
PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
XX Gorman JT;
XX
DR WPI; 1998-042117/04.

150202/60

```
XX Peptide(s) derived from specific region of respiratory syncytial
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
XX Example 4; Fig 12; 75pp: English.
XX
XX AAW39244-W39232 are derivatives of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 29 AA:
SQ
XX
XX Query Match 96.4%; Score 163; DB 19; Length 29;
XX Best Local Similarity 100.0%; Pred. No. 7.8e-16;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KORQNKPSKPNNDHFHEVNFVPCSTC 28
DB 1 kqrgnkpskpnndhfhevfnfvcpsc 28
XX
XX RESULT 2
XX ID AAW39245 standard; peptide; 42 AA.
XX AC AAW39245;
XX
XX DT 27-AUG-1998 (first entry)
XX
XX DE Human RSV G protein fragment (aa. 149-157) derivative #2.
XX
XX KW G protein; treatment; prevention; diagnosis; infection; immunity;
XX antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
XX OS Human respiratory syncytial virus.
XX
XX FH Key Location/Qualifiers
XX Modified-site 1
XX FT Disulfide-bond 25..38
XX FT Disulfide-bond 28..34
XX FT Modified-site 42
XX FT /note= "C-terminal amide"
XX
XX MO9746581-A1.
XX
XX PD 11-DEC-1997.
XX
XX PF 04-JUN-1997; 97MO-AU00351.
XX
XX PR 05-JUN-1996; 96AU-0000265.
XX
XX PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
XX PI Gorman JJ;
XX
XX DK WPI: 1998-042117/04.
XX
XX PT Peptide(s) derived from specific region of respiratory syncytial
XX virus G protein - used to treat, prevent, diagnose and immunise
XX PT against Pneumovirus infection
XX
XX PS Example 4; Fig 12; 75pp: English.
XX
```

```
CC AAW39244-W39232 are derivatives of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 42 AA:
SQ
XX
XX Query Match 96.4%; Score 163; DB 19; Length 42;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-15;
XX Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KORQNKPSKPNNDHFHEVNFVPCSTC 28
DB 1 kqrgnkpskpnndhfhevfnfvcpsc 28
XX
XX RESULT 3
XX ID AAW39217 standard; peptide; 49 AA.
XX AC AAW39217;
XX
XX DT 27-AUG-1998 (first entry)
XX
XX DE Human RSV A subtype G protein fragment (aa. 149-157) strain A2.
XX
XX KW G protein; treatment; prevention; diagnosis; infection; immunity;
XX antibody; Pneumovirus; identification; vaccine; cell receptor.
XX
XX OS Human respiratory syncytial virus.
XX
XX FH Key Location/Qualifiers
XX Modified-site 1
XX FT Disulfide-bond 25..38
XX FT Disulfide-bond 28..34
XX FT Modified-site 42
XX FT /note= "C-terminal amide"
XX
XX MO9746581-A1.
XX
XX PD 11-DEC-1997.
XX
XX PF 04-JUN-1997; 97MO-AU00351.
XX
XX PR 05-JUN-1996; 96AU 0000265.
XX
XX PA (BIOM-) BIOMOLECULAR RES INST LTD.
XX
XX PI Gorman JJ;
XX
XX DK WPI: 1998-042117/04.
XX
XX PT Peptide(s) derived from specific region of respiratory syncytial
XX virus G protein - used to treat, prevent, diagnose and immunise
XX PT against Pneumovirus infection
XX
XX PS Claim 5; Fig 2; 75pp: English.
XX
XX AAW39217-W39234 are fragments of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
XX Sequence 49 AA:
SQ
```

Query Match 96.4%; Score 163; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.3e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KORONKPPSKPNDHFHFVNFVPCISIC 28
 DB 1 Kqrqnkpsskpnndhfefvntfvpcisic 28

RESULT 4
 AAM39219
 ID AAM39219 standard; peptide: 49 AA.
 XX
 AC AAM39219;
 XX
 DT 27-AUG-1998 (first entry)
 XX
 DE Human RSV A subtype G protein fragment (aa. 149-157) strain A642.
 XX
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 XX
 PN MO9746581-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 04-JUN-1997; 97WO-AU00351.
 XX
 PR 05-JUN-1996; 96AU-0000265.
 XX
 PS (BIOM-) BIOMOLECULAR RES INST LTD.
 XX
 PT Gorman JJ;
 XX
 DT MPI: 1998-042117/04.
 XX
 DE Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 PS Claim 5; Fig 2; 75pp; English.
 PS
 CC AAM39217-W39234 are fragments of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to
 CC host cells and for characterisation of cell receptors for Pneumoviruses.
 CC When the fragments are used in combination with existing vaccines, they
 CC may allow a reduction in dose, and thus side effects, of the vaccine.
 CC
 XX
 SQ Sequence 49 AA:

Query Match 96.4%; Score 163; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.3e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KORONKPPSKPNDHFHFVNFVPCISIC 28
 DB 1 Kqrqnkpsskpnndhfefvntfvpcisic 28
 RESULT 5
 AAM39224

ID AAM39224 standard; peptide: 49 AA.
 XX
 AC AAM39224;
 XX
 DT 27-AUG-1998 (first entry)
 XX
 DE Human RSV A subtype G protein fragment (aa. 149-157) strain A1734.
 XX
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 XX
 PN MO9746581-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 04-JUN-1997; 97WO-AU00351.
 XX
 PR 05-JUN-1996; 96AU-0000265.
 XX
 PS (BIOM-) BIOMOLECULAR RES INST LTD.
 XX
 PT Gorman JJ;
 XX
 DT MPI: 1998-042117/04.
 XX
 DE Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 PS Claim 5; Fig 2; 75pp; English.
 PS
 CC AAM39217-W39234 are fragments of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to
 CC host cells and for characterisation of cell receptors for Pneumoviruses.
 CC When the fragments are used in combination with existing vaccines, they
 CC may allow a reduction in dose, and thus side effects, of the vaccine.
 CC
 XX
 SQ Sequence 49 AA:

Query Match 96.4%; Score 163; DB 19; Length 49;
 Best Local Similarity 100.0%; Pred. No. 1.3e-15;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KORONKPPSKPNDHFHFVNFVPCISIC 28
 DB 1 Kqrqnkpsskpnndhfefvntfvpcisic 28
 RESULT 6
 AAM39244
 ID AAM39244 standard; peptide: 49 AA.
 XX
 AC AAM39244;
 XX
 DT 27-AUG-1998 (first entry)
 XX
 DE Human RSV G protein fragment (aa. 149-157) derivative #1.
 XX
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.

XX	(BIOM-)	BIOMOLECULAR RES INST LTD.	
PA			
XX	Gorman JJ:		
P1			
XX			
DR	WPI: 1998-042117/04.		
XX			
XX	Peptide(s) derived from specific region of respiratory syncytial		
PT	virus(G protein - used to treat, prevent, diagnose and immunise		
PT	against Pneumovirus infection		
XX			
PS	Example 4; Fig 12; 75pp: English.		
XX			
CC	AAW39244-W39252 are derivatives of the human respiratory syncytial virus		
CC	(RSV) G protein corresponding to amino acids 149 to 197. These fragments		
CC	can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,		
CC	infection and to immunise against such infections. Antibodies raised		
CC	from these fragments may also be used diagnostically. The fragments may		
CC	also be used to identify compounds able to inhibit binding of RSV to		
CC	host cells and for characterisation of cell receptors for Pneumoviruses.		
CC	When the fragments are used in combination with existing vaccines, they		
CC	may allow a reduction in dose, and thus side effects, of the vaccine.		
XX			
SQ	Sequence 49 AA:		
	Query Match	96.4%; Score 163; DB 19; Length 49;	
	Best Local Similarity	100.0%; Pred. No. 1.3e-15;	
	Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.		
QY	1 KORONKPPSKPNDFHFEVFNFPSCIC 28		
Db	1 Kqrgnkpskpnndfhfadvfnvpsic 28		
RESULT 9			
AAW39251			
ID	AAW39251 standard; peptide: 49 AA.		
XX			
AC	AAW39251;		
XX			
DT	27-AUG-1998 (first entry)		
XX			
NE	Human RSV G protein fragment (aa. 149-157) derivative #8.		
XX			
XX	G protein; treatment; prevention; diagnosis; infection; immunity;		
XX	antibody; Pneumovirus; identification; vaccine; cell receptor.		
OS	Human respiratory syncytial virus.		
XX			
FT	Key	Location/Qualifiers	
FT	Modified-site	1	
FT		/note= "N-terminal blot group"	
FT	Disulfide-bond	25..38	
FT	Disulfide-bond	28..34	
FT	Modified-site	49	
FT		/note= "C-terminal amide"	
XX			
PN	WO9746581-A1.		
XX			
PD	11-DEC-1997.		
XX			
XX	04-JUN-1997; 97WO-AU00351.		
XX			
XX	05-JUN-1996; 96AU-0000265.		
XX			
XX	(BIOM-) BIOMOLECULAR RES INST LTD.		
XX			
XX	Gorman JJ;		
XX			
XX	WPI: 1998-042117/04.		
XX			
PT	Peptide(s) derived from specific region of respiratory syncytial		

```
PT virus G protein - used to treat, prevent, diagnose and immunise
PT against Pneumovirus infection
XX
PS Example 4; Fig 12; 75pp: English.
XX
CC AAN39244-W39252 are derivatives of the human respiratory syncytial virus
CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
CC infection and to immunise against such infections. Antibodies raised
CC from these fragments may also be used diagnostically. The fragments may
CC also be used to identify compounds able to inhibit binding of RSV to
CC host cells and for characterisation of cell receptors for Pneumoviruses.
CC When the fragments are used in combination with existing vaccines, they
CC may allow a reduction in dose, and thus side effects, of the vaccine.
XX
SQ Sequence 49 AA;

Query Match          96.4%; Score 163; DB 19; Length 49;
Best Local Similarity 100.0%; Pred. NO. 1.3e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 KORONKPPSPKPNNDPFHFEVFNFVPCSSIC 28
        |||||||
Db       1 kqrqnhkpskpndhfefvntfvpssic 28

RESULT 10
AAP70845
ID AAP70845 standard; protein; 298 AA.
XX
AC AAP70845;
XX
DT 05-APR-1991 (first entry)
XX
DE Sequence of human respiratory syncytial virus (HRSV) A2 strain
DE G protein.
XX
XX Vaccine.
XX
OS Human respiratory syncytial virus (HRSV).
XX
PN W08704I85-A.
PD 16-JUL-1987.
XX
PF 23-DEC-1986; 86WO-US02756.
XX
PR 14-JAN-1986; 86US-0818740.
XX
PA (UYNC-) UNIV OF N CAROLINA.
PA (WERT/) WERTZ G W.
PA (WERT/) WERTZ G W.
XX
WP1: 1987-206300/29.
DR N-PSDB; AAN70784.
XX
PT Vaccines for human respiratory virus - comprising proteins or
PT fragment encoded by a DNA sequence coding for human respiratory
PT syncytial virus proteins.
XX
PS Disclosure; Chart 13; 57pp: English.
XX
CC A novel plasmid which comprises a DNA sequence encoding this
CC protein, and the protein itself, are claimed, for use as HRSV
CC vaccines. The vaccine can be administered to pregnant women or to
CC women of child bearing age to stimulate maternal antibodies.
CC Infants can also be vaccinated at 2-3 months of age.
XX
SQ Sequence 298 AA;
```

Best Local Similarity 100.0%; Pred. No. 8.6e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNNDHFHFVFNFPSCIC 28
|||||
Db 149 kgqmkppskpndhfefvfnfvpsscic 176

RESULT 11

AAR25302
ID AAR25302 standard; Protein: 298 AA.

AC AAR25302;

DT 03-MAR-1993 (first entry)

DE HSRV glycoprotein G (gpg).

KM Vaccine: human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K;
KN major capsid protein; N.

OS Human respiratory syncytial virus strain A2.

PN US5149650-A.

PD 22-SEP-1992.

PF 14-JAN-1986; 86US-0818740.

PR 14-JAN-1986; 86US-0818740.

PR 13-JUL-1988; 88US-0218737.

PA (UYN-C) UNIV NORTH CAROLINA.

PI Collins PL, Wertz GW;

DR WPI: 1992-340247/41.

DR N-PSDB: AAQ29623.

PT Vaccines for human respiratory virus - include structural genes
PT coding for native structural viral proteins and immunogenic
PT fragments

PS Disclosure: Page 18; 21pp; English.

CC The sequences of mRNA encoding HRSV structural proteins are given in
CC AAQ29622-26. The proteins are F, G, 22K, 9.5K and major capsid
CC protein N. The sequences and encoded proteins are useful for
CC preparing vaccines against HRSV. The vaccines can be used to confer
CC immunity against respiratory tract infections on human subjects.

XX Sequence 298 AA;

XX

SO

Query Match 96.4%; Score 163; DB 13; Length 298;
Best Local Similarity 100.0%; Pred. No. 8.6e-15;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNNDHFHFVFNFPSCIC 28
|||||
Do 149 kgqmkppskpndhfefvfnfvpsscic 176

RESULT 12

AAW47605
ID AAW47605 standard; Protein: 298 AA.

AC AAW47605;

DT 11-JUN-1998 (first entry)

DE HRSV glycoprotein G.

XX

KM HRSV; glycoprotein F; gpf; glycoprotein G; gpg; vaccine.

OS Human respiratory syncytial virus.

PN US5716823-A.

PD 10-FEB-1998.

PE 12-MAY-1997; 97US-0854783.

PR 13-JUL-1988; 88US-0218737.

PR 14-JAN-1986; 86US-0818740.

PR 23-DEC-1986; 86WO-0502756.

PR 11-JUN-1992; 92US-0897171.

PR 12-MAY-1997; 97US-0854783.

PA (PHAA) PHARMACIA & UPJOHN CO.

PI Collins PL, Wertz GW;

DR WPI: 1998-144802/13.

DR N-PSDB: AAV18736.

PT Production of human respiratory syncytial virus glyco-protein F or G
PT - by culturing eukaryotic host cells transfected with corresponding
PT DNA

PS Example 1; Columns 27-28; 17pp; English.

CC The present sequence was used in the development of a novel method
CC for the production of human respiratory syncytial virus (HRSV)
CC glycoprotein F (gpf) or glycoprotein G (gpg). The method comprises
CC culturing eukaryotic host cells transfected with an isolated DNA
CC sequence encoding HRSV gpf or gpg. The gp can be used to prepare
CC vaccines against HRSV.

XX Sequence 298 AA;

XX

SO

Query Match 96.4%; Score 163; DB 19; Length 298;
Best Local Similarity 100.0%; Pred. No. 8.6e-15;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KORONKPPSKPNNDHFHFVFNFPSCIC 28
|||||

Db 149 kgqmkppskpndhfefvfnfvpsscic 176

RESULT 13
AAP90441
ID AAP90441 standard; protein: 681 AA.

AC AAP90441;

DT 01-NOV-1989 (first entry)

DE Chimeric human respiratory syncytial virus glycoproteins F and G.

CC Chimeric polypeptide: human respiratory syncytial virus;
CC protein F; protein G; vaccine.

XX Human respiratory syncytial virus.

XX

PN WO8905823-A.

PD 29-JUN-1989.

PE 31-OCT-1988; 88WO-US03784.

PR 23-DEC-1987; 87US-0137387.

PA (UPJO) UPJOHN CO.

P1 Mathen M;
 XX
 DK WPI: 1989-206593/28.
 XX
 PF Chimeric human respiratory syncytial virus polyprotein(s)
 PT - contg. immunogenic fragments from HRSV glycoproteins
 PT F and G, for vaccine prodn.
 XX
 PS Claim 3: page 47-48; 50pp; English.
 XX
 CC Chimeric polypeptide contg. a signal sequence and one or more
 CC immunogenic fragments from both human respiratory syncytial virus
 CC glycoproteins F and G. Can be used in vaccines. Hosts are, eg.
 CC E. coli, Chinese hamster ovary cells, murine C127 cells and
 CC S. frugiperda.
 XX
 SQ Sequence 681 AA:

 Query Match 96.4%; Score 163; DB 10; Length 681;
 Best Local Similarity 100.0%; Pred. No. 2e-14;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28
 ||||||||||||||||||||||||||||
 Db 543 KGRQKPKPKPNDHFHFVFNVPSCIC 570

 RESULT 14
 ID AAM39218 standard; peptide; 49 AA.
 XX
 AC AAM39218;
 XX
 DT 27-AUG-1998 (first entry)
 XX
 DE Human RSV A subtype G protein fragment (aa 149-157) strain long A.
 XX
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 XX
 PN MO9746581-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 04-JUN-1997; 97MO-AU00351.
 XX
 PR 05-JUN-1996; 96AU-0000265.
 XX
 PA (BIOM-) BIOMOLECULAR RES INST LTD.
 XX
 PI Gorman JJ;
 XX
 DR WPI: 1998-042117/04.
 XX
 PT Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 PS Claim 5; Fig 2; 75pp; English.
 XX
 CC AAM39217-W39234 are fragments of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to
 CC host cells and for characterisation of cell receptors for Pneumoviruses.
 CC When the fragments are used in combination with existing vaccines, they
 CC may allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 SQ Sequence 681 AA:

 Query Match 96.4%; Score 163; DB 10; Length 681;
 Best Local Similarity 100.0%; Pred. No. 2e-14;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28
 ||||||||||||||||||||||||||||
 Db 543 KGRQKPKPKPNDHFHFVFNVPSCIC 570

CC host cells and for characterisation of cell receptors for Pneumoviruses.
 CC When the fragments are used in combination with existing vaccines, they
 CC may allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 SQ Sequence 49 AA:

 Query Match 94.7%; Score 160; DB 19; Length 49;
 Best Local Similarity 96.4%; Pred. No. 3.5e-15;
 Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28
 ||||||||||||||||||||||||
 Db 1 KGRQKPKPKPNDHFHFVFNVPSCIC 28

 RESULT 15
 ID AAM39221 standard; peptide; 49 AA.
 XX
 AC AAM39221;
 XX
 DT 27-AUG-1998 (first entry)
 XX
 DE Human RSV A subtype G protein fragment (aa. 149-157) strain A6256.
 XX
 KW G protein; treatment; prevention; diagnosis; infection; immunity;
 KW antibody; Pneumovirus; identification; vaccine; cell receptor.
 XX
 OS Human respiratory syncytial virus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 25..38
 FT Disulfide-bond 28..34
 XX
 PN MO9746581-A1.
 XX
 PD 11-DEC-1997.
 XX
 PF 04-JUN-1997; 97MO-AU00351.
 XX
 PR 05-JUN-1996; 96AU-0000265.
 XX
 PA (BIOM-) BIOMOLECULAR RES INST LTD.
 XX
 PI Gorman JJ;
 XX
 DR WPI: 1998-042117/04.
 XX
 PT Peptide(s) derived from specific region of respiratory syncytial
 PT virus G protein - used to treat, prevent, diagnose and immunise
 PT against Pneumovirus infection
 XX
 PS Claim 5; Fig 2; 75pp; English.
 XX
 CC AAM39217-W39234 are fragments of the human respiratory syncytial virus
 CC (RSV) G protein corresponding to amino acids 149 to 197. These fragments
 CC can be used to treat, prevent or diagnose Pneumovirus, specifically RSV,
 CC infection and to immunise against such infections. Antibodies raised
 CC from these fragments may also be used diagnostically. The fragments may
 CC also be used to identify compounds able to inhibit binding of RSV to
 CC host cells and for characterisation of cell receptors for Pneumoviruses.
 CC When the fragments are used in combination with existing vaccines, they
 CC may allow a reduction in dose, and thus side effects, of the vaccine.
 XX
 SQ Sequence 49 AA:

 Query Match 94.7%; Score 160; DB 19; Length 49;
 Best Local Similarity 96.4%; Pred. No. 3.5e-15;
 Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28

Thu Sep 5 14:28:48 2002

us-09-202-035-39.rag

|||||:|||||
Db 1 kqrqkprnkpnndfnfeyfnfypsic 28

Search completed: September 4, 2002, 17:36:21
Job time: 255 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 4, 2002, 17:34:51 : Search time 14.76 Seconds
(without alignments)
188.793 Million cell updates/sec

Title: US-09-202-035-39

Perfect score: 169

Sequence: 1 KORONKPPSKPNNDHFHFVFNPCISIC 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	96.4	297	2 J01205	attachment protein
2	163	96.4	297	2 J01204	attachment protein
3	163	96.4	298	1 MGNZ	major surface glycoprotein
4	160	94.7	297	2 J01208	attachment protein
5	160	94.7	298	1 MGNZRL	major surface glycoprotein
6	160	94.7	298	2 J01207	attachment protein
7	160	94.7	298	2 J05680	G protein - Human
8	154	91.1	297	2 J01206	attachment protein
9	148	87.6	297	2 J01209	attachment protein
10	130	76.9	292	1 MGNZ18	major surface glycoprotein
11	130	76.9	292	1 MGNZ60	major surface glycoprotein
12	58	34.3	1861	2 T13845	microtubule-associ
13	57	33.7	1188	2 S48861	gene el protein -
14	55.5	32.8	263	2 J02388	glycoprotein G - O
15	55.5	32.8	263	2 A48732	attachment glycoprotein
16	54	32.0	160	2 B84947	signal peptidase I
17	54	32.0	274	2 AEO468	diaminopimelate ep
18	54	32.0	274	2 ACO919	diaminopimelate ep
19	54	32.0	275	1 S01913	diaminopimelate ep
20	54	32.0	275	2 C91221	diaminopimelate ep
21	54	32.0	275	2 F86067	diaminopimelate ep
22	54	32.0	427	2 T41257	hypothetical prote
23	52.5	31.1	257	1 MGNZBR	major surface glycoprotein
24	51	30.2	279	2 C70458	diaminopimelate ep
25	51	30.2	452	2 T33049	hypothetical prote
26	51	30.2	492	2 A71822	hypothetical prote
27	51	30.2	492	2 B69074	probable formate d
28	50.5	29.9	566	2 B53196	orphan hormone nuc
29	50.5	29.9	502	2 S49931	SVI protein - yea

30	50	29.6	96	2	H84381	hypothetical prote
31	50	29.6	290	2	G82360	diaminopimelate ep
32	50	29.6	398	2	D81397	probable periplasm
33	49.5	29.3	104	2	G84607	hypothetical prote
34	49.5	29.3	419	2	D86453	CDS protein F9L11..
35	48.5	28.7	633	2	T47524	hypothetical prote
36	48	28.4	340	2	F85256	hypothetical prote
37	48	28.4	513	2	T30733	A-type Inclusion b
38	48	28.4	661	2	A58768	ATP-dependent RNA
39	48	28.4	846	2	F75525	outer membrane pro
40	47.5	28.1	289	2	A82478	transposase all700
41	47.5	28.1	895	2	T45738	hypothetical prote
42	47	27.8	113	2	S43435	nuclear receptor p
43	47	27.8	212	2	G69838	hypothetical prote
44	47	27.8	388	2	T32994	hypothetical prote
45	47	27.8	455	2	J01224	nucleobindin precu

ALIGNMENTS

RESULT 1
J01205
attachment protein - human respiratory syncytial virus (strain RSB1734)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: J01205
R:Canine, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: J01204; MUID:91374005
A:Accession: J01205
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
infection and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 96.4%; Score 163; DB 2; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KORONKPPSKPNNDHFHFVFNPCISIC 28
DB 149 KORONKPPSKPNNDHFHFVFNPCISIC 176

RESULT 2
J01204
attachment protein - human respiratory syncytial virus (strain RSB642)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: J01204
R:Canine, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: J01204; MUID:91374005
A:Accession: J01204
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
infection and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predi

Query Match 96.4%; Score 163; DB 2; Length 297;

Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 28: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCISIC 28
|||||
Db 149 KORONKPPSKPNNDFHEVFNFVPCISIC 176

RESULT 3
MONZ
major surface glycoprotein G - human respiratory syncytial virus
C:Species: human respiratory syncytial virus
C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999
C:Accession: A94048; A93599; A04039
R:Wertz, G.W.; Collins, P.L.; Huang, Y.; Gruber, C.; Levine, S.; Ball, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985
A:Title: Nucleotide sequence of the G protein gene of human respiratory syncytial virus
A:Reference number: A94048; MUID:85216636
A:Accession: A94048
A:Molecule type: mRNA
A:Residues: 1-298 <WER>
A:Cross-references: GB:M11486; GB:K01459; GB:K02719; GB:K03348; GB:K03349; GB:M11217; GB:7.1; PID:9333932
A>Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid protein
R:Satake, M.; Collan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S.
Nucleic Acids Res. 13, 7795-7812, 1985
A:Title: Respiratory syncytial virus envelope glycoprotein (G) has a novel structure.
A:Reference number: A93599; MUID:86067198
A:Accession: A93599
A:Molecule type: mRNA
A:Residues: 1-298 <SAR>
A:Cross-references: GB:X03149; NID:960997; PIDN:CA26928.1; PID:960998
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:38-66/Domain: transmembrane #status predicted <TNM>
F:85.135,237,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 96.4%; Score 163; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.2e-15;
Matches 28: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCISIC 28
|||||
Db 149 KORONKPPSKPNNDFHEVFNFVPCISIC 176

RESULT 4
J01208
attachment protein - human respiratory syncytial virus (strain RSB6256)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: J01208
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: J01204; MUID:91374005
A:Accession: J01208
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract ill
children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85.103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 94.7%; Score 160; DB 2; Length 297;
Best Local Similarity 96.4%; Pred. No. 8.3e-15;
Matches 27: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCISIC 28
|||||
Db 149 KORONKPPSKPNNDFHEVFNFVPCISIC 176

RESULT 5
MONZRL
major surface glycoprotein G - human respiratory syncytial virus (strain Long)
C:Species: human respiratory syncytial virus
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: A32703; S12279
R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and
A:Reference number: A32703; MUID:87289657
A:Accession: A32703
A:Molecule type: mRNA
A:Residues: 1-298 <JOH>
A:Cross-references: GB:M17212; NID:9333940; PIDN:AAA47411.1; PID:9333941
R:Garcia-Barreno, B.; Portela, A.; Delgado, T.; Lopez, J.A.; Melero, J.A.
EMBO J. 9, 4181-4187, 1990
A:Title: Frame shift mutations as a novel mechanism for the generation of neutraliz
A:Reference number: S12279; MUID:91065351
A:Accession: S12279
A:Molecule type: mRNA
A:Residues: 1-298 <GAR>
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TNM>
F:85.103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 94.7%; Score 160; DB 1; Length 298;
Best Local Similarity 96.4%; Pred. No. 8.3e-15;
Matches 27: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCISIC 28
|||||
Db 149 KORONKPPSKPNNDFHEVFNFVPCISIC 176

RESULT 6
J01207
attachment protein - human respiratory syncytial virus (strain RSB6190)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: J01207
R:Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup
A:Reference number: J01204; MUID:91374005
A:Accession: J01207
A:Molecule type: mRNA
A:Residues: 1-298 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory trac
children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85.103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status pre

Query Match 94.7%; Score 160; DB 2; Length 298;
Best Local Similarity 96.4%; Pred. No. 8.3e-15;
Matches 27: Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCISIC 28
|||||
Db 149 KORONKPPSKPNNDFHEVFNFVPCISIC 176

RESULT 7

```
JC5680
C:Comment: Human respiratory syncytial virus
C:Species: Human respiratory syncytial virus
C:Date: 11-Nov-1997 #sequence_revision 11-Nov-1997 #text_change 26-Feb-1998
C:Accession: JC5680
R:Gen: X.; Wang, Z.; Qian, Y.; Zhu, R.; Deng, J.; Du, J.; Zhu, Z.
A:Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain 18
A:Reference number: JC5680
A:Accession: JC5680
A:Molecule type: mRNA
A:Residues: 1-298 <GEN>
A:Experimental source: strain B79
A:Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for res
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
F:1-38/Domain: intracellular #status predicted <INT>
F:39-66/Domain: transmembrane #status predicted <TMM>
F:67-298/Domain: extracellular #status predicted <EXC>

Query Match          94.7%; Score 160; DB 2; Length 298;
Best Local Similarity 96.4%; Pred. No. 8.3e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDHFENFVPCSTC 28
    |||||:|||||:|||||:|||||:
Db 149 KORONKPPSKPNNDHFENFVPCSTC 176

RESULT 8
JQ1206
attachment protein - human respiratory syncytial virus (strain RSB5857)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1206
R:Gen: P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1206
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>
C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract ill
children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match          91.1%; Score 154; DB 2; Length 297;
Best Local Similarity 92.9%; Pred. No. 5.7e-14;
Matches 26; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDHFENFVPCSTC 28
    |||||:|||||:|||||:|||||:
Db 149 KORONKPPSKPNNDHFENFVPCSTC 176

RESULT 9
JQ1209
attachment protein - human respiratory syncytial virus (strain RSB6614)
N:Alternate names: G protein
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C:Accession: JQ1209
R:Gen: P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2091-2096, 1991
A:Title: Identification of variable domains of the attachment (G) protein of subgroup A
A:Reference number: JQ1204; MUID:91374005
A:Accession: JQ1209
A:Molecule type: mRNA
A:Residues: 1-297 <CAN>

C:Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract
er children and adults.
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match          87.6%; Score 148; DB 2; Length 297;
Best Local Similarity 89.3%; Pred. No. 4e-13;
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDHFENFVPCSTC 28
    |||||:|||||:|||||:|||||:
Db 149 KORONKPPSKPNNDHFENFVPCSTC 176

RESULT 10
MGN218
major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
C:Accession: B32703
R:Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A:Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and
A:Reference number: A32703; MUID:87289657
A:Accession: B32703
A:Molecule type: mRNA
A:Residues: 1-292 <JOH>
A:Cross-references: GB:M17213; NID:q333942; PIDN:AAA7412.1; PID:q333943
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TMM>
F:81,86,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          76.9%; Score 130; DB 1; Length 292;
Best Local Similarity 72.4%; Pred. No. 1.3e-10;
Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDHFENFVPCSTC 29
    |||||:|||||:|||||:|||||:
Db 149 KSKKNPPKPKDDYDFEVENFVPCSTC 177

RESULT 11
MGN260
major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N:Alternate names: attachment glycoprotein G
C:Species: human respiratory syncytial virus
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: A37077
R:Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A:Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis
gous subgroup virus challenge.
A:Reference number: A37077; MUID:90357765
A:Accession: A37077
A:Molecule type: mRNA
A:Residues: 1-292 <SUL>
A:Cross-references: EMBL:M55633; NID:q333944; PIDN:AAA47413.1; PID:q333945
C:Genetics:
A:Gene: G
C:Superfamily: respiratory syncytial virus major surface glycoprotein G
C:Keywords: glycoprotein; transmembrane protein
F:41-63/Domain: transmembrane #status predicted <TMM>
F:81,86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          76.9%; Score 130; DB 1; Length 292;
Best Local Similarity 72.4%; Pred. No. 1.3e-10;
Matches 21; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

OY 1 KORONKPPSKPNNDFHEVFNFVPCISG 29
 DB 149 KSRKPKPKPKPDYHFEVFNFVPCISG 177

RESULT 12

T13845
 microtubule-associated protein - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
 C:Accession: T13845
 R:Saunders, R.D.; Avides, M.C.; Howard, T.; Gonzalez, C.; Glover, D.M.
 J. Cell Biol. 137, 881-890, 1997
 A:Title: The Drosophila gene abnormal spindle encodes a microtubule-associated protein
 A:Reference number: 217792; MUID:97296495
 A:Accession: T13845
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1861 <SAUV>
 A:Cross-references: EMBL:U95171; NID:q1930121; PID:q1930122; PIDN:AAB51540.1
 C:Genetics:
 A:Gene: asp
 A:Cross-references: FlyBase:FBgn0000140
 C:Function:
 A:Description: is required for the normal function of the mitotic spindle

Query Match 34.3%; Score 58; DB 2; Length 1861;
 Best Local Similarity 37.0%; Pred. No. 9.3;
 Matches 10; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCSI 27
 DB 1799 KONARKPPMTSGRYKSKQKINFTPCSL 1825

RESULT 13

S48861
 gene e1 protein - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C:Accession: S48861
 R:Nehls, M.; Pfeifer, D.; Lueno, K.; Boehm, T.
 Submitted to the EMBL Data Library, September 1994
 A:Description: A transcription map of the region flanked by betaa3-crystallin and neuro
 A:Reference number: S48861
 A:Accession: S48861
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1188 <NEH>
 A:Cross-references: EMBL:X81632

Query Match 33.7%; Score 57; DB 2; Length 1188;
 Best Local Similarity 42.3%; Pred. No. 8.2;
 Matches 11; Conservative 4; Mismatches 7; Indels 4; Gaps 1;

OY 4 ONKPPSKPNNDFHEVFNFV----PC 25
 DB 410 RNMPLKFKYHDFHSEIFQYTVWGPC 435

RESULT 14

JQ2388
 glycoprotein G - ovine respiratory syncytial virus
 C:Species: ovine respiratory syncytial virus
 C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 28-May-1999
 C:Accession: JQ2388
 R:Malipieddi, S.K.; Samal, S.K.
 J. Gen. Virol. 74, 2787-2791, 1993
 A:Title: Analysis of the ovine respiratory syncytial virus (RSV) G glycoprotein gene de
 A:Reference number: JQ2388; MUID:94103788
 A:Accession: JQ2388

A:Molecule type: mRNA
 A:Residues: 1-263 <MAL>
 A:Cross-references: GB:S67863; NID:q544771; PIDN:AAB29551.1; PID:q544773
 A:Experimental source: MSU 83-1578
 C:Superfamily: respiratory syncytial virus major surface glycoprotein G
 C:Keywords: glycoprotein; transmembrane protein
 F:1-37/Domain: Intracellular #status predicted <INT>
 F:38-64/Domain: transmembrane #status predicted <TM>
 F:65-263/Domain: extracellular #status predicted <EXT>

Query Match 32.8%; Score 55.5; DB 2; Length 263;
 Best Local Similarity 38.5%; Pred. No. 3;
 Matches 10; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
 OY 4 ONKPPSKPNNDFHEVFNFVPCISG 28
 DB 151 QKSNPSEIQDYSDFOILPYPCNIC 176

RESULT 15

A48732
 attachant glycoprotein G - ovine respiratory syncytial virus ORSV
 C:Species: ovine respiratory syncytial virus
 C:Date: 16-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
 C:Accession: A48732
 R:Alansari, H.; Potgieter, L.N.
 Virology 196, 873-877, 1993
 A:Title: Nucleotide sequence analysis of the ovine respiratory syncytial virus G gly
 A:Reference number: A48732; MUID:93383418
 A:Accession: A48732
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-263 <ALA>
 A:Note: sequence extracted from NCBI backbone (NCBIN:137891, NCBIPI:137894)
 C:Superfamily: respiratory syncytial virus major surface glycoprotein G

Query Match 32.8%; Score 55.5; DB 2; Length 263;
 Best Local Similarity 38.5%; Pred. No. 3;
 Matches 10; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

OY 4 ONKPPSKPNNDFHEVFNFVPCISG 28
 DB 151 QKSNPSEIQDYSDFOILPYPCNIC 176

Search completed: September 4, 2002, 17:37:03
 Job time: 132 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:35:51 ; Search time 10.34 Seconds

(without alignments)
108,594 Million cell updates/sec

Title: US-09-202-035-39

Perfect score: 169

Sequence: 1 KORONKPPSKPNDHFVFNFPVCSICG 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	96.4	297	1	VGLG_HRSV2
2	163	96.4	297	1	VGLG_HRSV3
3	163	96.4	298	1	VGLG_HRSV4
4	160	94.7	297	1	VGLG_HRSV5
5	160	94.7	298	1	VGLG_HRSV6
6	160	94.7	298	1	VGLG_HRSV7
7	154	91.1	297	1	VGLG_HRSV4
8	148	87.6	297	1	VGLG_HRSV7
9	130	76.9	292	1	VGLG_HRSV1
10	130	76.9	292	1	VGLG_HRSV8
11	55.5	32.8	263	1	VGLG_ORSVN
12	55	32.5	274	1	DAPE_PASMU
13	55	32.5	528	1	GD_DROME
14	54	32.0	160	1	LSPA_BUCAT
15	54	32.0	274	1	DAPE_ECOLI
16	54	32.0	274	1	DAPE_SALTY
17	54	32.0	274	1	DAPE_YERPE
18	53.5	31.7	835	1	UBPQ_MOUSE
19	52.5	31.1	257	1	VGLE_MOUSE
20	51	30.2	279	1	DAPE_AOUAE
21	50.5	29.9	556	1	RORA_HUMAN
22	50.5	29.9	902	1	SYGI_YEAST
23	48	28.4	661	1	VASH_DROME
24	48	28.4	805	1	TACI_HUMAN
25	47	27.8	459	1	NCBI_MOUSE
26	47	27.8	864	1	E78A_DROME
27	46	27.2	102	1	VE7_PAPVE
28	46	27.2	235	1	C554_NITEU
29	46	27.2	274	1	DAPE_NITEN
30	46	27.2	276	1	DAPE_PSEAE
31	46	27.2	312	1	KAPS_CATRO
32	46	27.2	432	1	MRJ1_APIME
33	46	27.2	586	1	KPCI_MOUSE

34	46	27.2	587	1	KPCI_HUMAN	P41743	homo sapien
35	46	27.2	845	1	MAT3_RAT	P43244	rattus norv
36	46	27.2	847	1	MAT3_HUMAN	P43243	homo sapien
37	46	27.2	2009	1	CINI_HUMAN	P35498	homo sapien
38	46	27.2	2009	1	CINI_RAT	P04774	rattus norv
39	45.5	26.9	727	1	CTCF_HUMAN	P49711	homo sapien
40	45.5	26.9	728	1	CTCF_CHICK	008705	gallus gall
41	45.5	26.6	168	1	NUE2_RHIME	P56310	Thizobium m
42	45	26.6	519	1	THRC_SOLTU	Q9mC28	solanum tub
43	45	26.6	731	1	YB88_YEAST	P38330	saccharomyc
44	45	26.6	752	1	CO2_HUMAN	P06681	homo sapien
45	45	26.6	794	1	PMS1_SCHPO	P54280	Schizosacch

ALIGNMENTS

RESULT 1	VGLG_HRSV2	STANDARD:	PRT:	297 AA.
ID	VGLG_HRSV2			
AC	P27021;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DE	Major surface glycoprotein G (Attachment glycoprotein G).			
GN	G.			
OS	Human respiratory syncytial virus (strain rsb642).			
OC	Viruses; ssRNA negative-strand viruses; Mononegavirales;			
OC	Parmyxoviridae; Pneumovirinae; Pneumovirus.			
OX	NCBI_TaxID=11252;			
RN	{1}			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-91374005; PubMed-1895054;			
RX	Cane P.A., Matthews D.A., Pringle C.R.;			
RT	"Identification of variable domains of the attachment (G) protein of			
RT	subgroup A respiratory syncytial viruses.";			
RL	J. Gen. Virol. 72:2091-2096(1991)			
CC	- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE			
CC	RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND			
CC	HEMAGGLUTININATING ACTIVITIES.			
CC	- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED			
CC	CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.			
CC	- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS			
CC	DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.			
DR	PIR; J01204; J01204.			
DR	InterPro: IPR000925; Glycoprot_G.			
DR	Plan: PF00802; Glycoprotein_G; 1.			
KW	Transmembrane; Glycoprotein.			
FT	DOMAIN 1 37			
FT	TRANSMEM 38 66			
FT	DOMAIN 67 297			
FT	CARBOHYD 135 135			
FT	CARBOHYD 144 144			
FT	CARBOHYD 237 237			
SO	SEQUENCE 297 AA; 32745 MW; FC72A7F5A8B8BF6C CRC64;			

Query Match

96.4%; Score 163; DB 1; Length 297;

Best Local Similarity 100.0%; Pred. No. 6.2e-15;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNDHFVFNFPVCSIC 28

DB 149 KORONKPPSKPNDHFVFNFPVCSIC 176

RESULT 2

VGLG_HRSV3 STANDARD; PRT; 297 AA.

AC P27022;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-AUG-1992 (Rel. 23, Last annotation update)

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DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G
OS Human respiratory syncytial virus (strain rsb1734).
OC Viruses: ssRNA negative-strand viruses: Mononegavirales;
OC Paramyxoviridae: Pneumovirinae: Pneumovirus.
OX NCBI_TaxID=11253;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR: J01205; J01205.
DR InterPro: IPR000925; Glycoprot-G.
DR Pfam: PF00802; Glycoprotein-G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 297 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 297 AA; 32525 MW; 48448FE091E1802 CRC64;

Query Match 96.4%; Score 163; DB 1; Length 297;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCISIC 28
DB 149 KORONKPPSKPNNDFHEVFNFVPCISIC 176

RESULT 3
VGIQ_HRSVA STANDARD: PRT: 298 AA.
AC P03423;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G
OS Human respiratory syncytial virus (strain A2).
OC Viruses: ssRNA negative-strand viruses: Mononegavirales;
OC Paramyxoviridae: Pneumovirinae: Pneumovirus.
OX NCBI_TaxID=11259;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85216636; PubMed=3858865;
RA Wertz G.W., Collins P.L., Huang Y., Gruber C., Levine S., Ball L.A.;
RT "Nucleotide sequence of the G protein gene of human respiratory
RT syncytial virus reveals an unusual type of viral membrane protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4075-4079(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86067198; PubMed=4069997;
RA Setake M., Colligan J.E., Elango N., Norby E., Venkatesan S.;
RT "Respiratory syncytial virus envelope glycoprotein (G) has a novel
RT structure.";
RL Nucleic Acids Res. 13:7795-7812(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=95266253; PubMed=7747420;
RA Connors M., Crowe J.E. Jr., Firestone C.Y., Murphy B.R., Collins P.L.;

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RT "A cold-passaged, attenuated strain of human respiratory syncytial
RT virus contains mutations in the F and L genes.";
RL Virology 208:478-484(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97187925; PubMed=9035372;
RA Crowe J.E. Jr., Firestone C.Y., Whitehead S.S., Collins P.L.,
RA Murphy B.R.;
RT "Acquisition of the ts phenotype by a chemically mutagenized cold-
RT passaged human respiratory syncytial virus vaccine candidate results
RT from the acquisition of a single mutation in the polymerase (L)
RT gene.";
RL Virus Genes 13:269-273(1996).
CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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DR EMBL: M1486; AA59857.1; -
DR EMBL: X03149; CA26928.1; -
DR EMBL: U50363; AAB86663.1; -
DR EMBL: U50363; AAB86675.1; -
DR EMBL: U63644; AAC55969.1; -
DR PIR: A04039; MGN2.
DR InterPro: IPR000925; Glycoprot-G.
DR Pfam: PF00802; Glycoprotein-G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 66 POTENTIAL.
FT DOMAIN 67 298 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 298 AA; 32586 MW; 993C3D2D68BC634 CRC64;

Query Match 96.4%; Score 163; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHEVFNFVPCISIC 28
DB 149 KORONKPPSKPNNDFHEVFNFVPCISIC 176

RESULT 4
VGIQ_HRSV6 STANDARD: PRT: 297 AA.
ID VGIQ_HRSV6
AC P27025;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G
OS Human respiratory syncytial virus (strain rsb6256).
OC Viruses: ssRNA negative-strand viruses: Mononegavirales;
OC Paramyxoviridae: Pneumovirinae: Pneumovirus.
OX NCBI_TaxID=11256;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;

```

RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses."
RL J. Gen. Virol. 72:2091-2096(1991).
CC -I- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR: J01208; J01208.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 66
FT DOMAIN 37 37
FT TRANSMEM 38 66
FT DOMAIN 37 37
FT TRANSMEM 38 66
FT CARBOHYD 103 103
FT CARBOHYD 135 135
FT CARBOHYD 237 237
FT CARBOHYD 251 251
FT CARBOHYD 294 294
SQ SEQUENCE 297 AA; 32708 MW; 6781756C38B64A80 CRC64;

Query Match 94.7%; Score 160; DB 1; Length 297;
Best Local Similarity 96.4%; Pred. No. 1.6e-14;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDHFEEVNFVPCISIC 28
DB 149 KORONKPPKPNNDHFEEVNFVPCISIC 176

RESULT 5
VGLG_HRSVL STANDARD; PRT; 298 AA.
AC P27024;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (strain r6b6190).
OC Viruses: ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374005; PubMed=1895054;
RA Cane P.A., Matthews D.A., Pringle C.R.;
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses."
RL J. Gen. Virol. 72:2091-2096(1991).
CC -I- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -I- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
DR PIR: J01207; J01207.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 66
FT DOMAIN 37 37
FT TRANSMEM 38 66
FT CARBOHYD 103 103
FT CARBOHYD 135 135
FT CARBOHYD 237 237
FT CARBOHYD 251 251
FT CARBOHYD 294 294
SQ SEQUENCE 294 AA; 32708 MW; 6781756C38B64A80 CRC64;

SQ SEQUENCE 298 AA; 32769 MW; 4D74EB54D34D7BA5 CRC64;

Query Match 94.7%; Score 160; DB 1; Length 298;
Best Local Similarity 96.4%; Pred. No. 1.6e-14;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDHFEEVNFVPCISIC 28
DB 149 KORONKPPKPNNDHFEEVNFVPCISIC 176

RESULT 6
VGLG_HRSVL STANDARD; PRT; 298 AA.
AC P20895;
DT 01-FEB-1991 (rel. 17, Created)
DT 01-FEB-1996 (rel. 33, Last sequence update)
DT 01-FEB-1996 (rel. 33, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN G.
OS Human respiratory syncytial virus (subgroup A / strain Long).
OC Viruses: ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11260;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289657; PubMed=2441388;
RA Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
RT "The G glycoprotein of human respiratory syncytial viruses of
RT subgroups A and B: extensive sequence divergence between
RT antigenically related proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
CC -I- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
CC HEMAGGLUTININATING ACTIVITIES.
CC SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M17212; AAA47411.1;
DR PIR: A32703; MGNZRL.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein_G; 1.
KW Transmembrane; Glycoprotein.
FT DOMAIN 1 37
FT TRANSMEM 38 66
FT DOMAIN 37 37
FT TRANSMEM 38 66
FT CARBOHYD 103 103
FT CARBOHYD 135 135
FT CARBOHYD 237 237
FT CARBOHYD 251 251
FT CARBOHYD 294 294
SQ SEQUENCE 298 AA; 32781 MW; B79FEFA4B4A73B0E CRC64;

Query Match 94.7%; Score 160; DB 1; Length 298;
Best Local Similarity 96.4%; Pred. No. 1.6e-14;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDHFEEVNFVPCISIC 28
DB 149 KORONKPPKPNNDHFEEVNFVPCISIC 176

RL	J. Gen Virol.	72:2091-2096(1991).
CC	- FUNCTION:	UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
CC	HEMAGGLUTININATING ACTIVITIES.	
CC	SUBCELLULAR LOCATION:	EXPRESSED ON THE SURFACE OF THE INFECTED
CC	CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.	
CC	- PTM:	MAV CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
CC	DISTRIBUTION:	AMONG THE 91 SERINE AND THREONINE RESIDUES.
CC	PIR:	JOI209; JOI209.
DR	InterPro:	IPRO00925: Glycoprot.G.
DR	Pfam:	PF00802: Glycoprotein.G; 1.
KW	Transmembrane:	Glycoprotein.
FT	DOMAIN	1 37 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	38 66 POTENTIAL.
FT	DOMAIN	67 297 EXTRACELLULAR (POTENTIAL).
FT	CARBOHYD	103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	251 251 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	297 AA; 32670 MW; 58B38402BE437ACD CRC64;
Query Match 87.6%; Score 148; DB 1; Length 297;		
Best Local Similarity 89.3%; Pred. No. 6; 5e-13;		
Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps		
Oy	1 KORONKPPSKPNNDPEFEVENFVPCSGC 28	
Db	149 KOHONKRPKNRNHNHFVEVFNPFCSTIC 176	
RESULT 9	VGIG_HRSV1	
ID	VGIG_HRSV1	STANDARD: PRT: 292 AA.
AC	P20896;	
DT	01-FEB-1991 (Rel. 17, Created)	
DT	01-FEB-1991 (Rel. 17, Last sequence update)	
DT	01-NOV-1991 (Rel. 20, Last annotation update)	
DE	Major surface glycoprotein G (Attachment glycoprotein G).	
GN	Human respiratory syncytial virus (subgroup B / strain 18537).	
OS	Viruses: ssRNA negative-strand viruses: Mononegavirales:	

```

Oy      1 KORONKPPSKPNNDHFENVFVPCISIC 28
        ||| | :||| | ||| | | | | | | | |
Db      149 KQHNKKPKNKHNNHFFHEVFENFPCCSIC 176

Query Match          87.6% Score 148; DB 1; Length 297;
Best Local Similarity 89.3%; Pred.No. 6,5e-13;
Matches    25; Conservative   1; Mismatches     2; Indels       0; Gaps       0;

RESULT      9
VGLG_HRSVL ID VGLG_HRSVL STANDARD: PRT: 292 AA.
AC P20896;
DT 01-FEB-1991 (Rel. 17, Created)
DI 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1991 (Rel. 20, Last annotation update)
DE Major surface glycoprotein G (Attachment glycoprotein G).
GN Human respiratory syncytial virus (subtype B / strain 18537).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11251;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87289657; Pubmed=2441388;
RA Johnson P.R., Spriggs M.K., Olmsted R.A., Collins P.L.;
RT "The glycoprotein of human respiratory syncytial viruses of
  subgroups A and B: extensive sequence divergence between
  antigenically related proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 84:5625-5629(1987).
RC -I- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
  RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
  HEMAGGLUTININATING ACTIVITIES.
CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
CC -I- PMM MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
  DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
-----
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-----
DR EMBL: MJ1713; AAAA7412.1; -.
DR PIR: B32703; MCN218.
DR InterPro: IPR000925; Glycoprot_G.
DR Pfam: PF00802; Glycoprotein.G.1.
```

KM Transmembrane: Glycoprotein.
 FT DOMAIN 1 37
 FT TRANSMEM 38 66
 FT DOMAIN 67 292
 FT CARBOHYD 81 81
 FT CARBOHYD 86 86
 FT CARBOHYD 100 100
 SQ SEQUENCE 292 AA: 32306 MW: 80859.69 CA7AFC2 CRC64:

Query Match
 Best Local Similarity 76.9%: Score 130: DB 1: Length 292:
 Matches 21: Conservative 2: Mismatches 6: Indels 0: Gaps 0:

QY 1 KORONKPPSKPNNDFHEVFNFPVCSICG 29
 DB 149 KSRKSNPKPKKDDYHFEVFNFPVCSICG 177

RESULT 10
 VGLG_HRSV8 STANDARD: PRT: 292 AA.
 ID VGLG_HRSV8
 AC P23041:
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-AUG-1992 (Rel. 23, Last annotation update)
 DE Major surface glycoprotein G (Attachment glycoprotein G).
 GN G.
 OS Human respiratory syncytial virus (subgroup B / strain 8/60).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=11258;
 RX MEDLINE-90357765; PubMed-1697126;
 RA Sullender W.M., Anderson K., Wertz G.W.;
 RT "The respiratory syncytial virus subgroup B attachment glycoprotein:
 RT analysis of sequence, expression from a recombinant vector, and
 RT evaluation as an immunogen against homologous and heterologous
 RT subgroup virus challenge."
 RT Virology 178:195-203(1990).
 RL [2]
 RN RP SEQUENCE FROM N.A.
 RP MEDLINE-91374595; PubMed-1895391;
 RA Sullender W.M., Wilson M.M., Anderson L.J., Wertz G.W.;
 RT Genetic diversity of the attachment protein of subgroup B
 RT respiratory syncytial viruses."
 RT J. Virol. 65:5425-5434(1991).
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS
 CC DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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 CC EMBL: M55633; AAA47413.1;
 DR EMBL: W73545; AAA47408.1;
 DR PIR: A37077; MCN260.
 DR InterPro: IPR000925; Glycoprot.G.
 DR Pfam: PF00802; Glycoprotein_G.1.
 DR Transmembrane: Glycoprotein.
 KM DOMAIN 1 37
 FT TRANSMEM 38 66
 FT DOMAIN 67 292
 FT CARBOHYD 81 81
 FT CARBOHYD 86 86
 FT CARBOHYD 100 100
 SQ SEQUENCE 292 AA: 32306 MW: 80859.69 CA7AFC2 CRC64:

FT CARBOHYD 81 81
 FT CARBOHYD 86 86
 FT CARBOHYD 100 100
 SQ SEQUENCE 292 AA: 32143 MW: 80859.69 CA7AFC2 CRC64:

Query Match
 Best Local Similarity 76.9%: Score 130: DB 1: Length 292:
 Matches 21: Conservative 2: Mismatches 6: Indels 0: Gaps 0:

QY 1 KORONKPPSKPNNDFHEVFNFPVCSICG 29
 DB 149 KSRKSNPKPKKDDYHFEVFNFPVCSICG 177

RESULT 11
 VGLG_ORSVW STANDARD: PRT: 263 AA.
 ID VGLG_ORSVW
 AC O86695:
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Major surface glycoprotein G (Attachment glycoprotein G).
 GN G.
 OS Ovine respiratory syncytial virus (strain MSU 83-1578) (ORSV).
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
 OX NCBI_TaxID=79699;
 RX MEDLINE-94103788; PubMed-8277288;
 RA Mallipedi S.K., Samal S.K.;
 RT "Analysis of the ovine respiratory syncytial virus (RSV) G
 RT glycoprotein gene defines a subgroup of ungulate RSV."
 RT J. Gen. Virol. 74:2787-2791(1993).
 CC -1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
 CC RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
 CC HEMAGGLUTININATING ACTIVITIES.
 CC -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED
 CC CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
 CC -1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
 CC HRS VIRUS.
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 CC EMBL: S67863; AAB29551.1;
 DR EMBL: S67862; AAB29551.1; JOINED.
 DR HSSP: P22261; IBRV.
 DR InterPro: IPR000925; Glycoprot.G.
 DR Pfam: PF00802; Glycoprotein_G.1.
 DR Transmembrane: Glycoprotein.
 KM DOMAIN 1 37
 FT TRANSMEM 38 66
 FT DOMAIN 67 263
 FT DISULFID 173 186
 FT DISULFID 176 182
 FT CARBOHYD 85 85
 FT CARBOHYD 97 97
 FT CARBOHYD 97 97
 FT CARBOHYD 234 234
 FT CARBOHYD 251 251
 SQ SEQUENCE 263 AA: 29225 MW: 81A6496047B3B71 CRC64:

Query Match
 Best Local Similarity 32.8%: Score 55.5: DB 1: Length 263:
 Matches 10: Conservative 6: Mismatches 9: Indels 1: Gaps 1:

OY 4 QNKPSPKNNDF-HFEVFNFPSCIC 28
 DB 151 OKSNPSEIQDYSDFOLIPVPCNIC 176

RESULT 12
 DAPF_PASMU STANDARD: PRT: 274 AA.
 ID DAPF_PASMU STANDARD: PRT: 274 AA.
 AC P57962;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase).
 GN DAPF OR PM1703.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Pasteurella.
 OX NCBI_TaxId=747;
 RN 11;
 RP SEQUENCE FROM N.A.
 RC STRAIN-PM70;
 RX MEDLINE-21145866; PubMed-11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida pm70.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -1- CATALYTIC ACTIVITY: L-2,6-diaminoheptanedioate - meso-
 CC -1- diaminoheptanedioate.
 CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF LYSINE FROM ASPARTATE
 CC -1- SEMIALDEHYDE.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE DIAMINOPIMELATE EPIMERASE FAMILY.
 CC
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 CC
 CC EMBL: AE006206; AAK03787.1;
 DR InterPro: IPR001653; DAP_epimerase.
 DR Pfam: PF01678; DAP_epimerase; 1.
 DR PROSITE: PS01326; DAP_EPIMERASE; 1.
 KW Isomerase; Lysine biosynthesis; Complete proteome.
 FT ACT_SITE 73 73 BY SIMILARITY.
 FT ACT_SITE 217 217 BY SIMILARITY.
 FT SEQUENCE 274 AA; 30184 MW; 84F7FMA1B372C38C CRC64;

Query Match 32.5%; Score 55; DB 1: Length 274;
 Best Local Similarity 50.0%; Pred. No. 2;
 Matches 8: Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 6 KPSPKNNDFEVEN 21
 DB 49 EPPYDPDLDFHFRIFN 64

RESULT 13
 GD DROME STANDARD: PRT: 528 AA.
 AC O62589;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine protease gd precursor (EC 3.4.21.-) (Gastrulation defective
 DE protein).
 GN GD OR CG1505.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxId=7227;
 RN 11;
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE=Embryo;
 RX MEDLINE-98284015; PubMed-9618496;
 RA Konrad K.D., Goralski T.J., Mahowald A.P., Marsh J.L.;
 RT "The gastrulation defective gene of Drosophila melanogaster is a
 RT member of the serine protease superfamily.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:6819-6824(1998).
 RN 12;
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Fertler S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hristova M., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA LaRo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Stump R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Wortley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith R.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- FUNCTION: PART OF A CASCADE THAT ACTIVATES THE SPZ LIGAND FOR THE
 CC TL RECEPTOR IN THE VENTRAL REGION OF THE EGG. GD ACTS EARLY TO
 CC ESTABLISH A LOCALIZED COMPLEX INVOLVING OTHER PUTATIVE PROTEASES
 CC (EA, SNK AND NDL) THAT LEAD TO LOCALIZED ACTIVATION OF SPZ. LOSS
 CC OF GD FUNCTION RESULTS IN A DORSALIZED ACTIVITY OF SPZ. LOSS
 CC -1- DEVELOPMENTAL STAGE: OVARY AND EARLY EMBRYO. EXPRESSION REGIONS IN
 CC PREVITELLOGENIC STAGES AND IS SEEN IN GERM LINE-DETAILED NURSE
 CC CELLS OF THE GERMARIUM. EXPRESSION CONTINUES THROUGHOUT COGNESIS
 CC WITH TRANSCRIPTS FROM THE NURSE CELLS ACCUMULATING IN THE OOCYTES.
 CC MOST ABUNDANT IN THE OVARIES. THE LEVEL OF PROTEIN DECREASES FROM
 CC THE MOMENT OF EGG LAYING AND IS ESSENTIALLY GONE BY 4HR.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY. STRONGEST TO OTHER GRANZYMES AND TO MAST CELL
 CC PROTEASES.
 CC
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CC -----
DR EMBL: AF056311; AAC13558.1;
DR EMBL: AE003487; AAF48122.1;
DR EMBL: U09808; AAC24235.1;
DR HSSP: P00734; 1B7X.
DR FlyBase: FBgn0000808; qd.
DR InterPro: IPR001254; trypsin.
DR Pfam: PF00089; trypsin.1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR SMART: SM00020; TRYP-SPC.1.
DR PROSITE: PS50240; TRYPsin.DOM.1.
DR PROSITE: PS00134; TRYPsin.HIS.1.
DR PROSITE: PS00135; TRYPsin.SER; FALSE_NEG.
DR HydroBase: serine protease; Glycoprotein; Developmental protein;
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 528 SERINE PROTEASE GD.
FT DOMAIN 243 528 SERINE PROTEASE.
FT ACT_SITE 292 347 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 347 347 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 468 468 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 277 293 BY SIMILARITY.
FT DISULFID 429 446 BY SIMILARITY.
FT CARBOHYD 269 269 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 528 AA; 59084 MW; 31E3EBBC5AE07A8 CRC64;

Query Match 32.5%; Score 55; DB 1; Length 528;
Best Local Similarity 37.9%; Pred. NO. 3.9;
Matches 11; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDHFHFVPCISIG 29
: : ||||| : : : |||||
Db 158 RKTDDKPPSTPHIQKKKPPAQAKKEICG 186

RESULT 14
LSPA_BUCAI STANDARD; PRT; 160 AA.
AC P57248;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal
DE peptidase) (Signal peptidase II) (Spsae II).
GN LSPA OR Bu148.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RX MEDLINE=20445173; PubMed=10993077;
RA Sugaenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS."
RL Nature 407:81-86(2000).
CC -!- FUNCTION: THIS PROTEIN SPECIFICALLY CATALYZES THE REMOVAL OF
CC SIGNAL PEPTIDES FROM PROLIPOPROTEINS (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
CC membrane poliproteins. Hydrolyses Xaa-Xbb-Xbb'-1-Cys, in which
CC Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc
CC is often Gly or Ala, and the Cys is alkylated on sulfur with a
CC diacylglyceryl group.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A8.
CC -----
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CC -----
DR EMBL: AF001118; BAB12866.1;
DR InterPro: IPR001872; Lipo_sig_Ptase.
DR Pfam: PF01252; Peptidase_A8.1.
DR PRINTS: PR00781; LIPOSIGPTASE.
DR PROSITE: PS00855; SPASE-II.1.
KW HydroBase: Aspartyl protease; Transmembrane; Complete proteome.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 72 92 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT TRANSMEM 134 154 POTENTIAL.
FT ACT_SITE 116 116 BY SIMILARITY.
FT ACT_SITE 143 143 BY SIMILARITY.
SQ SEQUENCE 160 AA; 18712 MW; 3485846DE9651D CRC64;

Query Match 32.0%; Score 54; DB 1; Length 160;
Best Local Similarity 60.0%; Pred. NO. 1.6;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 13 NDFHFVFNFPVPCSI 27
: : ||| : : |||
Db 132 NDWHFATFNINDCSI 146

RESULT 15
DAPF_ECOLI STANDARD; PRT; 274 AA.
AC P08885; P78126;
DT 01-NOV-1988 (Rel. 09, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diaminopimelate epimerase (EC 5.1.1.7) (DAP epimerase).
GN DAPF OR B3809.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RX MEDLINE=98057481; PubMed=1057443;
RA Richard C., Pritz C.;
RT "Nucleotide sequence of the dapF gene and flanking regions from
RT Escherichia coli K12."
RL Nucleic Acids Res. 16:10367-10367(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=92358234; PubMed=1379743;
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT "Analysis of the Escherichia coli genome: DNA sequence of the region
RT from 84.5 to 86.5 minutes."
RL Science 257:771-778(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [4]
RP SEQUENCE OF 259-274 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91072248; PubMed=2254268;
RA Colsons S.D., Sykora P., Szatmari G., Sherratt D.J.;
```

RT "Recombination at COLE1 cer requires the Escherichia coli xerc gene
RT product, a member of the lambda integrase family of site-specific
RT recombinases.";
RL J. Bacteriol. 172:6973-6980(1990).
RN (5)
RP SEQUENCE OF 1-8 FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97028791; PubMed-8874804;
RA Tiolot P., Sismeyro O., Vivares C., Glaser P., Bresson-Roy A.,
RA Danchin A.;
RT "Comparative analysis of the cya locus in enterobacteria and related
RT Gram-negative facultative anaerobes.";
RL Biochimie 78:277-287(1996).
CC -1- CATALYTIC ACTIVITY: L-L-2,6-diaminoheptanedioate = meso-
CC -1- diaminoheptanedioate.
CC -1- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF LYSINE FROM ASPARTATE
CC SEMIALDEHYDE.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE DIAMINOPIMELATE EPIMERASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: X12968; CAA31413.1; ALT_INIT.
DR EMBL: M87049; AAA67605.1; ALT_INIT.
DR EMBL: AE000457; AAC76812.1; ALT_INIT.
DR EMBL: M38257; AAA24761.1; -
DR EMBL: X66782; CAA47282.1; -
DR PIR: S01913; S01913.
DR PIR: A37841; A37841.
DR PIR: S30699; S30699.
DR PIR: S24977; S24977.
DR HSSP: P44859; 1BWZ.
DR Ecocore: EC10709; ddpf.
DR InterPro: IPR001653; DAP_epimerase.
DR Pfam: PF01678; DAP_epimerase; 1.
DR ProSite: PS01326; DAP_EPIMERASE; 1.
KW Isomerase; Lysine biosynthesis; Complete proteome.
FT ACT_SITE 73 73 BY SIMILARITY.
FT ACT_SITE 217 217 T -> S (IN REF. 3).
FT CONFLICT 98 98 CV -> WL (IN REF. 1).
FT CONFLICT 160 161 EH -> DD (IN REF. 1).
FT CONFLICT 200 201
SQ SEQUENCE 274 AA; 30222 MW; 489C112F785E8710 CRC64;

Query Match 32.0%; Score 54; DB 1; Length 274;
Best Local Similarity 50.0%; Pred. No. 2.7;
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 6 KPSPKPNNDHFHEVEN 21
: 11 1 111 : 11
DB 49 EPPYDELDHFYKIFN 64

Search completed: September 4, 2002, 17:37:51
Job time: 120 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:35:31 ; Search time 24.96 Seconds

(without alignments)
200.996 Million cell updates/sec

Title: US-09-202-035-39

Perfect score: 169
Sequence: 1 KORONKPPSKPNNDFHEVFVPCISICG 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	96.4	292	12	Q9YVB2 human respi
2	163	96.4	293	12	Q9YVB3 human respi
3	163	96.4	295	12	Q86356 respiratory
4	163	96.4	295	12	Q86360 respiratory
5	163	96.4	297	12	Q82066 human respi
6	163	96.4	297	12	Q82067 human respi
7	163	96.4	297	12	Q82071 human respi
8	163	96.4	297	12	Q9YVB5 human respi
9	160	94.7	278	12	Q9G6U1 human respi
10	160	94.7	278	12	Q9G6T7 human respi
11	160	94.7	278	12	Q9G6T4 human respi
12	160	94.7	278	12	Q9G6T3 human respi
13	160	94.7	278	12	Q9G6T0 human respi
14	160	94.7	279	12	Q9G6U0 human respi
15	160	94.7	279	12	Q9G6T9 human respi
16	160	94.7	279	12	Q9G6T8 human respi

17	160	94.7	279	12	Q9G6T5 human respi
18	160	94.7	279	12	Q9G6T2 human respi
19	160	94.7	279	12	Q9G6S9 human respi
20	160	94.7	279	12	Q9G6S8 human respi
21	160	94.7	279	12	Q9G6S7 human respi
22	160	94.7	279	12	Q9G6S6 human respi
23	160	94.7	279	12	Q9G6S0 human respi
24	160	94.7	279	12	Q9G6R9 human respi
25	160	94.7	292	12	Q9YVB0 human respi
26	160	94.7	293	12	Q9YVB1 human respi
27	160	94.7	295	12	Q86359 respiratory
28	160	94.7	296	12	Q86358 respiratory
29	160	94.7	297	12	Q82074 human respi
30	160	94.7	297	12	Q82078 human respi
31	160	94.7	297	12	Q82057 human respi
32	160	94.7	297	12	Q82058 human respi
33	160	94.7	298	12	Q82061 human respi
34	160	94.7	298	12	Q82073 human respi
35	160	94.7	298	12	Q82075 human respi
36	160	94.7	298	12	Q82076 human respi
37	160	94.7	298	12	Q82062 human respi
38	160	94.7	298	12	Q82065 human respi
39	160	94.7	298	12	Q82068 human respi
40	160	94.7	298	12	Q82056 human respi
41	160	94.7	298	12	Q82060 human respi
42	160	94.7	298	12	Q91945 human respi
43	160	94.7	298	12	Q9YVB4 human respi
44	160	94.7	298	12	Q09719 respiratory
45	160	94.7	298	12	Q09634 human respi

ALIGNMENTS

RESULT 1
Q9YVB2 PRELIMINARY; PRT; 292 AA.
ID Q9YVB2;
AC Q9YVB2;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WV19983;
RX MEDLINE=99022964; Pubmed=9806017;
RA Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of group A respiratory syncytial viruses that have caused repeat infections in children".
RT J. Infect. Dis. 178:925-932(1998).
RL EMBL: AF065408; AAD02944.1;
DR InterPro: IPR003880; Glycoprotei.G.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein.G; 1.
DR PRINTS: PRO1217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
FT NON_TER
FT 1
SQ SEQUENCE 292 AA; 31964 MW; 8942A8DD0A402A4B CRC64;

Query Match 96.4%; Score 163; DB 12; Length 292;
Best local Similarity 100.0%; Pred. No. 1..1e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFVPCISIC 28
DB 144 KORONKPPSKPNNDFHEVFVPCISIC 171

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RESULT      2
Q9YVB3      PRELIMINARY;      PRT:      293 AA.
AC      Q9YVB3;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      ATTACHMENT GLYCOPROTEIN G (FRAGMENT).
OS      Human respiratory syncytial virus.
OC      Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC      Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX      NCBI_TaxID=11250;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-WV6973;
RX      MEDLINE=99022964; PubMed=9806017;
RA      Sullender W.M., Mufson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT      "Antigenic and genetic diversity among the attachment proteins of
RT      group A respiratory syncytial viruses that have caused repeat
RT      infections in children."
RL      J. Infect. Dis. 178:925-932(1998).
DR      EMBL; AF065407; AAD02943.1; -.
DR      InterPro: IPR000925; Glycoprot_G.
DR      InterPro: IPR003880; Phosphopant_attach.
DR      Pfam: PF00802; Glycoprotein_G.1.
DR      PRINTS: PR01217; PRICHEXTNSN.
DR      PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT      NON_TER      1
SQ      SEQUENCE      293 AA; 32125 MW; 17B5B43396A63CCF CRC64;

Query Match      96.4%; Score 163; DB 12; Length 293;
Best Local Similarity 100.0%; Prd. No. 1.1e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KORONKPPSKPNNDHFHFVFNFPCCSIC 28
Db      144 KORONKPPSKPNNDHFHFVFNFPCCSIC 171
      |||||||
      |||||||

RESULT      3
Q86356      PRELIMINARY;      PRT:      295 AA.
AC      Q86356;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      G PROTEIN (FRAGMENT).
OS      respiratory syncytial virus.
OC      Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC      Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX      NCBI_TaxID=12814;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-RS89-1734;
RX      MEDLINE=91374005; PubMed=1895054;
RA      Cane P.A., Matthews D.A., Pringle C.R.;
RT      "Identification of variable domains of the attachment (G) protein of
RT      subgroup A respiratory syncytial viruses."
RL      J. Gen. Virol. 72:2091-2096(1991).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-RS89-1734;
RA      Cane P.A.;
RX      Submitted (APR-1993) to the EMBL/Genbank/DBJ databases.
DR      EMBL: X73350; CAAS1761.1; -.
DR      InterPro: IPR000925; Glycoprot_G.
DR      InterPro: IPR003880; Phosphopant_attach.
DR      Pfam: PF00802; Glycoprotein_G.1.
DR      PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.

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FT  NON TERM      1      1
SQ  SEQUENCE      295 AA: 32527 MW: D32BE769E0A23CFA CRC64:

Query Match          96.4%; Score 163; DB 12; Length 295;
Best Local Similarity 100.0%; Pred. NO. 1.1e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KORONKPPSKPNNDFHEVFENFVPCISIC 28
      |||||||
DB      147 KORONKPPSKPNNDFHEVFENFVPCISIC 174

RESULT 4
O86360
O86360 PRELIMINARY: PRT: 295 AA.
AC O86360:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE G PROTEIN (FRAGMENT)
OS respiratory syncytial virus.
OC Viruses: ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=12814;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RS89-642;
RX MEDLINE=91374005; PubMed=1895054;
RT "Cane P.A., Matthews D.A., Pringle C.R.,
RT "Identification of variable domains of the attachment (G) protein of
RT subgroup A respiratory syncytial viruses.";
RL J. Gen. Virol. 72:2091-2096(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-RS89-642;
RX
RL Cane P.A.;
RA Submitted (APR-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: X73354; CAAS1765.1; -
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam: PF00802; Glycoprotein_G_1
DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; UNKNOWN_1.
DR NON-TER 1
SQ SEQUENCE 295 AA: 32306 MW: 671DC044157D284 CRC64:

Query Match          96.4%; Score 163; DB 12; Length 295;
Best Local Similarity 100.0%; Pred. NO. 1.1e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KORONKPPSKPNNDFHEVFENFVPCISIC 28
      |||||||
DB      147 KORONKPPSKPNNDFHEVFENFVPCISIC 174

RESULT 5
O82066
O82066 PRELIMINARY: PRT: 297 AA.
AC O82066:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN.
OS Human respiratory syncytial virus.
OC Viruses: ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUBGROUP A;
RX MEDLINE=94335057; PubMed=8057427;

```

RA Garcia O., Martin M., Dopazo J., Arbizu J., Fabrasile S., Russi J.,
RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
RA Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
RT A): cocirculating lineages and correlation of genetic and antigenic
RT changes in the G glycoprotein.";
RL J. Virol. 68:5448-5459(1994).
DR EMBL: Z33427; CAAB3870.1; -;
DR InterPro: IPR000925; Glycoprot_G.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam: PF00802; Glycoprotein_G. 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.
SQ SEQUENCE 297 AA; 32589 MW; F210F8C681935DD CRC64;

Query Match 96.4%; Score 163; DB 12; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28
Db 149 KORONKPPSKPNDHFHFVFNVPSCIC 176

RESULT 6
Q82067 PRELIMINARY; PRT; 297 AA.
AC Q82067;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUBGROUP A;
RX MEDLINE=94335057; Pubmed=8057427;
RA Garcia O., Martin M., Dopazo J., Arbizu J., Fabrasile S., Russi J.,
RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
RA Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
RT A): cocirculating lineages and correlation of genetic and antigenic
RT changes in the G glycoprotein.";
RL J. Virol. 68:5448-5459(1994).
DR EMBL: Z33428; CAAB3871.1; -;
DR InterPro: IPR000925; Glycoprot_G.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam: PF00802; Glycoprotein_G. 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.
SQ SEQUENCE 297 AA; 32555 MW; 9D0A69BECABEB6C8 CRC64;

Query Match 96.4%; Score 163; DB 12; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28
Db 149 KORONKPPSKPNDHFHFVFNVPSCIC 176

RESULT 7
Q82071 PRELIMINARY; PRT; 297 AA.
AC Q82071;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN.

GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUBGROUP A;
RX MEDLINE=94335057; Pubmed=8057427;
RA Garcia O., Martin M., Dopazo J., Arbizu J., Fabrasile S., Russi J.,
RA Hortal M., Perez-Brena P., Martinez I., Garcia-Barreno B.,
RA Melero J.A.;
RT "Evolutionary pattern of human respiratory syncytial virus (subgroup
RT A): cocirculating lineages and correlation of genetic and antigenic
RT changes in the G glycoprotein.";
RL J. Virol. 68:5448-5459(1994).
DR EMBL: Z33432; CAAB3875.1; -;
DR InterPro: IPR000925; Glycoprot_G.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam: PF00802; Glycoprotein_G. 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.
SQ SEQUENCE 297 AA; 32581 MW; AD947B2318193306 CRC64;

Query Match 96.4%; Score 163; DB 12; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28
Db 149 KORONKPPSKPNDHFHFVFNVPSCIC 176

RESULT 8
Q9YVB5 PRELIMINARY; PRT; 297 AA.
AC Q9YVB5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ATTACHMENT GLYCOPROTEIN G.
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WV2780;
RX MEDLINE=99022964; Pubmed=9806017;
RA Sullender W.M., Mutson M.A., Prince G., Anderson L.J., Wertz G.W.;
RT "Antigenic and genetic diversity among the attachment proteins of
RT group A respiratory syncytial viruses that have caused repeat
RT infections in children.";
RL J. Infect. Dis. 178:925-932(1998).
DR EMBL: AF065405; AAD02941.1; -;
DR InterPro: IPR000925; Glycoprot_G.
DR InterPro: IPR003880; Phosphopant_attach.
DR InterPro: IPR002965; P-rich_extensn.
DR Pfam: PF00802; Glycoprotein_G. 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.
SQ SEQUENCE 297 AA; 32572 MW; SC10E719405EF5C1 CRC64;

Query Match 96.4%; Score 163; DB 12; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.2e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNDHFHFVFNVPSCIC 28
Db 149 KORONKPPSKPNDHFHFVFNVPSCIC 176


```
RESULT 9
090601 ID 090601 PRELIMINARY: PRT: 278 AA.
AC 090601:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-91142;
RX MEDLINE-20283719; PubMed-10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea."
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193305; AAF23728.1; -
DR InterPro: IPR000925; Glycoprot_G.
DR InterPro: IPR003880; Phosphopantl_attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein_G. 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA: 30461 MW; AC113DCDCFF47EDE CRC64;

Query Match 94.7%; Score 160; DB 12; Length 278;
Best Local Similarity 96.4%; Pred. No. 2.9e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHFVFNVPSCIC 28
Db 130 KORONKPPKPNNDHFHFVFNVPSCIC 157

RESULT 10
0906T7 ID 0906T7 PRELIMINARY: PRT: 278 AA.
AC 0906T7:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-92308;
RX MEDLINE-20283719; PubMed-10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea."
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193309; AAF23732.1; -
DR InterPro: IPR000925; Glycoprot_G.
DR InterPro: IPR003880; Phosphopantl_attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein_G. 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA: 30547 MW; B33F085F89E1A9D0 CRC64;

Query Match 94.7%; Score 160; DB 12; Length 278;
Best Local Similarity 96.4%; Pred. No. 2.9e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHFVFNVPSCIC 28
Db 130 KORONKPPKPNNDHFHFVFNVPSCIC 157

RESULT 11
0906T4 ID 0906T4 PRELIMINARY: PRT: 278 AA.
AC 0906T4:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-92528;
RX MEDLINE-20283719; PubMed-10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
RT consecutive epidemics in Korea."
RL J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193312; AAF23735.1; -
DR InterPro: IPR000925; Glycoprot_G.
DR InterPro: IPR003880; Phosphopantl_attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein_G. 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
FT NON_TER 1
SQ SEQUENCE 278 AA: 30474 MW; 2E05963863BF8A75 CRC64;

Query Match 94.7%; Score 160; DB 12; Length 278;
Best Local Similarity 96.4%; Pred. No. 2.9e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDFHFVFNVPSCIC 28
Db 130 KORONKPPKPNNDHFHFVFNVPSCIC 157

RESULT 12
0906T3 ID 0906T3 PRELIMINARY: PRT: 278 AA.
AC 0906T3:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID=11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-93006;
RX MEDLINE-20283719; PubMed-10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of
RT subgroups A and B of respiratory syncytial virus isolated over 9
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RT consecutive epidemics in Korea."
J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193313; AAF23736.1; .
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam: PF00802; Glycoprotein.G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
RT NON_TER 1
FT SEQUENCE 278 AA: 30443 MW: 8E2974FE2E1AE15C9 CRC64;

Query Match 94.7%; Score 160; DB 12; Length 278;
Best Local Similarity 96.4%; Pred. No. 2.9e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFNFPVCSIC 28
DB 130 KORONKPPSKPNNDFHEVFNFPVCSIC 157

RESULT 13
ID 0906T0 PRELIMINARY; PRT; 278 AA.
AC 0906T0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID-11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-94191;
RC MEDLINE-20283719; PubMed-10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea."
J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193316; AAF23739.1; .
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Phosphopant_attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein.G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
RT NON_TER 1
FT SEQUENCE 278 AA: 30440 MW: 8D38997DEB9A6292 CRC64;

Query Match 94.7%; Score 160; DB 12; Length 278;
Best Local Similarity 96.4%; Pred. No. 2.9e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFNFPVCSIC 28
DB 130 KORONKPPSKPNNDFHEVFNFPVCSIC 157

RESULT 14
ID 0906U0 PRELIMINARY; PRT; 279 AA.
AC 0906U0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.

OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID-11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-91242;
RC MEDLINE-20283719; PubMed-10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea."
J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193306; AAF23729.1; .
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Phosphopant_attach.
DR Pfam: PF00802; Glycoprotein.G; 1.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
RT NON_TER 1
FT SEQUENCE 279 AA: 30544 MW: 6B270AAEB1CB3533 CRC64;

Query Match 94.7%; Score 160; DB 12; Length 279;
Best Local Similarity 96.4%; Pred. No. 2.9e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFNFPVCSIC 28
DB 130 KORONKPPSKPNNDFHEVFNFPVCSIC 157

RESULT 15
ID 0906T9 PRELIMINARY; PRT; 279 AA.
AC 0906T9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOPROTEIN (FRAGMENT).
GN G.
OS Human respiratory syncytial virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Pneumovirinae; Pneumovirus.
OX NCBI_TaxID-11250;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-91399;
RC MEDLINE-20283719; PubMed-10823752;
RA Choi E.H., Lee H.J.;
RT "Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea."
J. Infect. Dis. 181:1547-1556(2000).
DR EMBL: AF193307; AAF23730.1; .
DR InterPro: IPR000925; Glycoprot.G.
DR InterPro: IPR003880; Phosphopant_attach.
DR InterPro: IPR002965; P_rich_extensn.
DR Pfam: PF00802; Glycoprotein.G; 1.
DR PRINTS: PR01217; PRICHEXTENS.
DR PROSITE: PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
RT NON_TER 1
FT SEQUENCE 279 AA: 30570 MW: AE6CF9C1D8F8A97C CRC64;

Query Match 94.7%; Score 160; DB 12; Length 279;
Best Local Similarity 96.4%; Pred. No. 2.9e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFNFPVCSIC 28
DB 130 KORONKPPSKPNNDFHEVFNFPVCSIC 157

Thu Sep 5 14:28:50 2002

us-09-202-035-39.rspt

Page 6

Search completed: September 4, 2002, 17:37:34
Job time: 123 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 17:34:06 : Search time 13.01 Seconds

(Without alignments)
54.446 Million cell updates/sec

Title: US-09-202-035-39

Perfect score: 169

Sequence: 1 KORONKPPSKPNNDPHEVFNPCISIC 29

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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6: /cgn2_6/prodata/2/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	163	96.4	681	5194595-19	Patent No. 5194595
2	160	94.7	298	US-08-467-963C-8	Sequence 8, Appli
3	160	94.7	298	US-08-838-189D-8	Sequence 8, Appli
4	160	94.7	298	US-08-852-344D-8	Sequence 8, Appli
5	160	94.7	298	US-08-344-639E-8	Sequence 8, Appli
6	160	94.7	298	US-08-467-969A-8	Sequence 8, Appli
7	160	94.7	298	US-08-467-961A-8	Sequence 8, Appli
8	160	94.7	298	US-08-001-554A-8	Sequence 8, Appli
9	146	86.4	26	US-08-750-624-9	Sequence 9, Appli
10	115	68.0	37	US-08-793-792-12	Sequence 12, Appli
11	114	67.5	32	US-08-793-792-8	Sequence 8, Appli
12	109	64.5	28	US-08-793-792-4	Sequence 4, Appli
13	106	62.7	32	US-08-793-792-7	Sequence 7, Appli
14	106	62.7	37	US-08-793-792-11	Sequence 11, Appli
15	101	59.8	28	US-08-793-792-3	Sequence 3, Appli
16	60	35.5	30	US-08-836-504A-5	Sequence 5, Appli
17	50.5	29.9	556	US-09-106-194-3	Sequence 3, Appli
18	48.5	28.7	115	US-08-540-406-8	Sequence 8, Appli
19	48.5	28.7	115	US-08-656-055-8	Sequence 8, Appli
20	48.5	28.7	115	US-08-954-668-8	Sequence 8, Appli
21	48.5	28.7	115	PCT-US95-13233-8	Sequence 8, Appli
22	46	27.2	28	US-08-793-792-2	Sequence 2, Appli
23	46	27.2	32	US-08-793-792-6	Sequence 6, Appli
24	46	27.2	37	US-08-793-792-10	Sequence 10, Appli
25	46	27.2	310	US-08-605-284B-13	Sequence 13, Appli
26	46	27.2	587	US-08-313-274-2	Sequence 2, Appli
27	45.5	26.9	4	US-09-346-510B-23	Sequence 23, Appli

28	45.5	26.9	52	4	US-09-346-510B-22	Sequence 22, Appli
29	45.5	26.9	154	4	US-08-871-732A-1	Sequence 1, Appli
30	45.5	26.9	154	4	US-09-346-510B-1	Sequence 1, Appli
31	45.5	26.9	727	2	US-08-475-844-9	Sequence 9, Appli
32	45.5	26.9	727	2	PCT-US95-08429-9	Sequence 9, Appli
33	45.5	26.9	728	2	US-08-475-844-5	Sequence 5, Appli
34	45.5	26.9	728	3	PCT-US95-08429-5	Sequence 5, Appli
35	45	26.6	309	3	US-08-605-284B-4	Sequence 4, Appli
36	45	26.6	456	4	US-08-858-207A-366	Sequence 366, Appli
37	44.5	26.3	149	3	US-08-836-236-9	Sequence 9, Appli
38	44.5	26.3	476	4	US-08-134-557D-2	Sequence 2, Appli
39	44.5	26.3	477	4	US-09-128-142-2	Sequence 2, Appli
40	44.5	26.3	505	4	US-09-128-142-4	Sequence 4, Appli
41	44	26.0	309	3	US-08-605-284B-5	Sequence 5, Appli
42	44	26.0	309	3	US-08-605-284B-6	Sequence 6, Appli
43	44	26.0	310	3	US-08-605-284B-10	Sequence 10, Appli
44	44	26.0	310	3	US-08-605-284B-14	Sequence 14, Appli
45	44	26.0	310	3	US-08-605-284B-15	Sequence 15, Appli

ALIGNMENTS

RESULT 1
5194595-19
Patent No. 5194595
APPLICANT: MATTHEW, MICHAEL W.
TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING
IMMUNOGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/543,780
FILING DATE: 31-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 137,387
FILING DATE: 23-DEC-1987
SEQ ID NO:19:
LENGTH: 681
5194595-19

Query Match 96.4%: Score 163; DB 6; Length 681;
Best Local Similarity 100.0%: Pred. No. 2.3e-15;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KORONKPPSKPNNDPHEVFNPCISIC 28
Db 543 KORONKPPSKPNNDPHEVFNPCISIC 570

RESULT 2
US-08-467-963C-8
Sequence 8, Application US/08467963C
Patent No. 5968776
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: DU, Run-Pan
APPLICANT: EMASISHYN, Mary E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & Mcburney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APR-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-474 MIS:jdb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-467-963C-8

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Query Match	94.7%	Score 160;	DB 2;	Length 298;
Best Local Similarity	96.4%	Pred. No. 2.5e-15;		
Matches 27; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

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QY      1 KQRQNKPPSKPNNDFHFEVFNVPSCIC 28
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Db      149 KQRQNKPPSKPNNDFHFEVFNVPSCIC 176
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RESULT 3
 US-08-838-189D-8
 Sequence 8, Application US/08838189D
 Patent No. 5998169
 GENERAL INFORMATION:
 APPLICANT: KLEIN, Michel H
 APPLICANT: DU, Run-Pan
 APPLICANT: EMASYSHYN, Mary E
 TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
 CHIMERIC PROTEIN WHICH CONFERNS PROTECTION AGAINST
 TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Slim & McBurney
 STREET: 6th Floor, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1R7
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/838.189D
 FILING DATE: 16-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/001,554
 FILING DATE: 06-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9200117.1
 FILING DATE: 06-JAN-1992

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: ATTORNEY/AGENT INFORMATION:
: NAME: STEWART, Michael I
: REGISTRATION NUMBER: 24,973
: REFERENCE/DOCKET NUMBER: 1038-687 MIS:jh
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 595-1155
: TELEFAX: (416) 595-1163
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 298 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: US-08-838-189D-8

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Query Match	94.7%	Score 160;	DB 2;	Length 298;
Best Local Similarity	96.4%	Pred. No. 2.5e-15;		
Matches 27; Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy      1 KORONKPPSKPNNDFFHEVEFNVPSCIC 28
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Db     149 KORONKPPKPNNDFFHEVEFNVPSCIC 176
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RESULT 4
 US-08-852-344D-8
 : Sequence 8, Application US/08052344D
 : Patent No. 6017539
 : GENERAL INFORMATION:
 : APPLICANT: KLEIN, Michel H
 : APPLICANT: DU, Run-Pan
 : APPLICANT: EMASHYHN, Mary E
 : TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION
 : TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
 : TITLE OF INVENTION: SYNCTIAL VIRUS
 : NUMBER OF SEQUENCES: 37
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Sim & McBurney
 : STREET: 6th Floor, 330 University Avenue
 : CITY: Toronto
 : STATE: Ontario
 : COUNTRY: Canada
 : ZIP: M5G 1R7
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/852,344D
 : FILING DATE: 07-MAY-1997
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/344,639
 : FILING DATE: 14-NOV-1994
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: GB 9200117.1
 : FILING DATE: 06-JAN-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: STEWART, Michael I
 : REGISTRATION NUMBER: 24,973
 : REFERENCE/DOCKET NUMBER: 1038-688 MIS:jb
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (416) 595-1155
 : TELEFAX: (416) 595-1165
 : INFORMATION FOR SEQ ID NO: 8:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 298 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 US-08-852-344D-8

Query Match 94.7%; Score 160; DB 3; Length 298;
Best Local Similarity 96.4%; Pred. No. 2.5e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFNFPVCSIC 28
|||||:|||||:|||||:|||||:|||||
DB 149 KORONKPPKPNNDHFHEVFNFPVCSIC 176

RESULT 5

US-08-344-639E-8
; Sequence 8, Application US/08344639E
; Patent No. 6033668
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasysbyn, Mary E
; TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERES
; TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
; TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,639E
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-391 MIS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-639E-8

Query Match 94.7%; Score 160; DB 3; Length 298;
Best Local Similarity 96.4%; Pred. No. 2.5e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFNFPVCSIC 28
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DB 149 KORONKPPKPNNDHFHEVFNFPVCSIC 176

RESULT 6

US-08-467-969A-8
; Sequence 8, Application US/08467969A
; Patent No. 6168786
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasysbyn, Mary E
; TITLE OF INVENTION: Chimeric Immunogens
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 330 University Avenue, 6th Floor
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,969A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/001,554
; FILING DATE: 06-JAN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9200117.1
; FILING DATE: 06-JAN-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-475 MIS:db
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; TELEX: 065-24567 SIMBAS
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 298 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-467-969A-8

Query Match 94.7%; Score 160; DB 4; Length 298;
Best Local Similarity 96.4%; Pred. No. 2.5e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPPSKPNNDFHEVFNFPVCSIC 28
|||||:|||||:|||||:|||||:|||||
DB 149 KORONKPPKPNNDHFHEVFNFPVCSIC 176

RESULT 7

US-08-467-961A-8
; Sequence 8, Application US/08467961A
; Patent No. 6171783
; GENERAL INFORMATION:
; APPLICANT: Klein, Michel H
; APPLICANT: Du, Run-Pan
; APPLICANT: Ewasysbyn, Mary E
; TITLE OF INVENTION: Chimeric Immunogens
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Slim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467.961A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001.554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-476 MIS:bn
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-467-961A-8

Query Match 94.7%; Score 160; DB 4; Length 298;
Best Local Similarity 96.4%; Pred. No. 2.5e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOROKPPSKPNDFHFVFNVPSCIC 28
|||||:|||||:|||||:|||||
DB 149 KOROKPPSKPNDFHFVFNVPSCIC 176

RESULT 8
US-08-001-554A-8
Sequence 8, Application US/08001554A
Patent No. 6225091
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/001.554A
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-286
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
US-08-001-554A-8

Query Match 94.7%; Score 160; DB 4; Length 298;
Best Local Similarity 96.4%; Pred. No. 2.5e-15;
Matches 27; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOROKPPSKPNDFHFVFNVPSCIC 28
|||||:|||||:|||||:|||||
DB 149 KOROKPPSKPNDFHFVFNVPSCIC 176

RESULT 9
US-08-750-624-9
Sequence 9, Application US/08750624
Patent No. 6290971
GENERAL INFORMATION:
APPLICANT: Kandil, Ali
APPLICANT: James, Olive A
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
TITLE OF INVENTION: ADJUVANT COMPOSITIONS COMPRISING A
MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750.624
FILING DATE: 26-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-660
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-750-624-9

Query Match 86.4%; Score 146; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.8e-14;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KORONKPSKPNNDHFVEVNFVPC 25
|||||
Db 2 KORONKPSKPNNDHFVEVNFVPC 26

RESULT 10

US-08-793-792-12
; Sequence 12, Application US/08793792
; Patent No. 6077511

; GENERAL INFORMATION:

; APPLICANT:
; TITLE OF INVENTION: Antigenic peptides derived from the
; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,792

; FILING DATE:

; CLASSIFICATION: 514

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 37 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHEICAL: NO

US-08-793-792-12

Query Match 68.0%; Score 115; DB 3; Length 37;
Best Local Similarity 95.0%; Pred. No. 6.6e-10;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 SKPNDFHFEVNFVPC 28
:|||||
Db 1 KPNNDHFVEVNFVPC 20

RESULT 11

US-08-793-792-8
; Sequence 8, Application US/08793792
; Patent No. 6077511

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Antigenic peptides derived from the

; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,792

; FILING DATE:

; CLASSIFICATION: 514

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 32 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
US-08-793-792-8

Query Match 67.5%; Score 114; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 7.8e-10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KPNNDHFVEVNFVPC 28
|||||
Db 1 KPNNDHFVEVNFVPC 19

RESULT 12

US-08-793-792-4
; Sequence 4, Application US/08793792
; Patent No. 6077511

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Antigenic peptides derived from the

; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,792

; FILING DATE:

; CLASSIFICATION: 514

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHEICAL: NO

US-08-793-792-4

Query Match 64.5%; Score 109; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.3e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 PNNDHFVEVNFVPC 28
|||||
Db 1 PNNDHFVEVNFVPC 18

RESULT 13

US-08-793-792-7
; Sequence 7, Application US/08793792
; Patent No. 6077511

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Antigenic peptides derived from the

; TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis
; TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection.
; NUMBER OF SEQUENCES: 13

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/793,792

; FILING DATE:

; CLASSIFICATION: 514


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: INFORMATION FOR SEQ ID NO: 7:
:
: SEQUENCE CHARACTERISTICS:
:
:   LENGTH: 32 amino acids
:   TYPE: amino acid
:   STRANDEDNESS: single
:   TOPOLOGY: linear
:
: MOLECULE TYPE: peptide
:
: HYDROPHILIC: NO
:
: US-08-793-792-7

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Query Match	62.7%	Score 106	DB 3	Length 32
Best Local Similarity	85.0%	Prod. No.	1,1e-08	
Matches 17, Conservative		Mismatches	1	Gaps 0

```
Qy      10 KPNNDFHEFVFNVPSCIG 29
          || : || || || || || || ||
Db      1 KPKDDYHFEVFNVPSCIG 20
```

Query Match	62.7%	Score 106	DB 3	Length 37
Best Local Similarity	85.0%	Pred No. 1.2e+08		
Matches 17	Conservative 2	Mismatches 1	Indels 0	Gaps 0

```
QY      10 KPNNDHFEEVFNVPSCICG 29
          11 : : : : : : : : : :
Db       2 KPKDDYHFEEVFNVPSCICG 21
```

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: SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/793,792
:
: FILING DATE:
:
: CLASSIFICATION: 514
:
: INFORMATION FOR SEQ ID NO: 3:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 28 amino acids
:
: TYPE: amino acid
:
: STRANDEDNESS: single
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: peptide
:
: HYPOTHEICAL: NO
:
US-08-793-792-3

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Query Match	59.8%	Score 101	DB 3	Length 28
Best Local Similarity	84.2%	Pred. No.	4.7e-08	
Matches	16	Conservative	2	Mismatches 1
				Indels 0
				Caps 0

```
QY      11 PNDHFHEVENFVPCISIG 29  
         | :|:|||||||  
Db       1 PKDDYHFEVFNVPCSIG 19
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